



39780-1216R1C1D5 SAVED NOV 1 2005.TXT

SEQUENCE LISTING

<110> Ashkenazi, Avi J.  
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Tumas, Daniel  
Wood, William I.

<120> COMPOUNDS, COMPOSITIONS AND METHODS FOR  
THE TREATMENT OF DISEASES CHARACTERIZED BY A-33 RELATED  
ANTIGENS

<130> 39780-1216R1C1D5

<140> US 10/785,607

<141> 2004-02-24

<150> US 09/953,499

<151> 2001-09-14

<150> US 09/254,465

<151> 1999-03-05

<150> PCT/US98/24855

<151> 1998-11-20

<150> PCT/US98/19437

<151> 1998-09-17

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1

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<212> PRT

<213> Homo sapiens

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35 40 45  
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
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Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80  
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95  
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
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Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
115 120 125  
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
130 135 140  
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
145 150 155 160  
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn

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      165      170      175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
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      195      200      205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
      210      215      220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
      225      230      235
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
      245      250      255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
      260      265      270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
      275      280      285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
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      35      40      45
Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
      50      55      60
Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
      65      70      75      80
Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
      85      90      95
Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
      100      105      110
Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
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Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
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Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg
      145      150      155      160
Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile
      165      170      175
Trp Tyr Lys Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
      180      185      190
Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
      195      200      205
Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
      210      215      220
Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
      225      230      235
Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
      245      250      255
Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
      260      265      270
Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile
      275      280      285
Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile
      290      295      300

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 gcttggtcct ccatccaagc ctacagttaa catccccctc tctgccacca ttgggaaccg 180  
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 ctgacatgct cagaacaaga tggttcccc ccttctgaat acacctgggt caaagatggg 600  
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 gactcctgat ggcaaccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180  
 ctctgtctcc aagccacag tgacaactgg cagcggttat ggcttcacgg tgccccaggg 240  
 aatgaggatt agccttcaat gccagggttc ggggttctcc tccatcagt tatatttggg 300  
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ccaggaaaga gcctgcctgt ctttgccatc atcctcatca tctccttggtg ctgtatgggtg 660
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gaagcagcca gggcacatgc cagagaggcc aacgactctg gagaaaccat gaggggtggcc 780
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Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
35      40      45
Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
50      55      60
His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
65      70      75      80
His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
85      90      95
Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
100     105     110
Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
115     120     125
Thr Lys Ser Arg Val Arg Leu Val Leu Val Pro Pro Ser Lys Pro
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145     150     155     160
Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
165     170     175
Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
180     185     190
Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
195     200     205
Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
210     215     220
Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
225     230     235     240
Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
245     250     255
Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
260     265     270
Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
275     280     285
Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
290     295     300

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<212> DNA  
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&lt;210&gt; 9

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

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Lys Asp Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
35      40      45
Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
50      55      60
Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
65      70      75      80
Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
85      90      95
Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
100     105     110
Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
115     120     125
Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
130     135     140
Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
145     150     155     160
Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
165     170     175
Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
180     185     190
Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
195     200     205
Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
210     215     220
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
225     230     235     240
Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
245     250     255
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
260     265     270
Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
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&lt;210&gt; 10

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 <213> Mus musculus

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Cys Thr Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Val
 50      55      60
Gln Gly Ser Thr Thr Ala Leu Val Cys Tyr Asn Ser Gln Ile Thr Ala
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Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Ser Gly Ile Thr Phe Ser
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100      105      110
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130      135      140
Gly Asn Arg Ala Val Leu Thr Cys Ser Glu His Asp Gly Ser Pro Pro
145      150      155      160
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165      170      175
Ala Lys Lys Thr Arg Ala Phe Met Asn Ser Ser Phe Thr Ile Asp Pro
180      185      190
Lys Ser Gly Asp Leu Ile Phe Asp Pro Val Thr Ala Phe Asp Ser Gly
195      200      205
Glu Tyr Tyr Cys Gln Ala Gln Asn Gly Tyr Gly Thr Ala Met Arg Ser
210      215      220
Glu Ala Ala His Met Asp Ala Val Glu Leu Asn Val Gly Gly Ile Val
225      230      235      240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Leu Leu Ile Phe Gly
245      250      255
Val Trp Phe Ala Tyr Ser Arg Gly Tyr Phe Glu Thr Thr Lys Lys Gly
260      265      270
Thr Ala Pro Gly Lys Lys Val Ile Tyr Ser Gln Pro Ser Thr Arg Ser
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<210> 11  
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 <212> DNA  
 <213> Homo sapiens

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cagaggctga ggcaggcggg tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtcatgc ctgtagtccc 1800
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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Primer

<400> 12

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24

<210> 13

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Hybridization Probe

<400> 13

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<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Primer

<400> 14

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<210> 15

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<212> DNA

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<220>

<223> Synthetic Oligonucleotide Primer

<400> 15

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<400> 21  
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<210> 22  
<211> 50  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Hybridization Probe

<400> 22  
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<210> 23  
<211> 260  
<212> PRT  
<213> Homo sapiens

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35 40 45  
Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val  
50 55 60  
Thr Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp  
65 70 75 80  
Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr  
85 90 95  
Gly Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro  
100 105 110  
Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val Leu  
115 120 125  
Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe  
130 135 140  
Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr Arg Ala Phe  
145 150 155 160  
Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe  
165 170 175  
Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr Ser Cys Glu Ala Arg  
180 185 190  
Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala  
195 200 205  
Val Glu Arg Asn Val Gly Val Ile Val Ala Ala Val Leu Val Thr Leu  
210 215 220  
Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg  
225 230 235 240  
Gly His Phe Asp Arg Thr Lys Lys Gly Thr Ser Ser Lys Lys Val Ile  
245 250 255  
Tyr Ser Gln Pro  
260

<210> 24  
<211> 270  
<212> PRT  
<213> Homo sapiens

<400> 24

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20      25      30
Thr Ser Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu
35      40      45
Leu Thr His Thr Glu Arg Val Ile Trp Pro Phe Ser Asn Lys Asn
50      55      60
Tyr Ile His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn
65      70      75      80
Ala Glu Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala
85      90      95
Asp Asn Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu
100     105     110
Gly Asn Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser
115     120     125
Lys Pro Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile
130     135     140
Gln Leu Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser
145     150     155     160
Trp Lys Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro
165     170     175
Ala Ser Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser
180     185     190
Gly Tyr Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys
195     200     205
Asn Ile Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr
210     215     220
Val Gly Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile
225     230     235     240
Ile Ile Tyr Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp
245     250     255
Lys Glu Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro
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<210> 25  
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20      25      30
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35      40      45
Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu
50      55      60
Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr
65      70      75      80
Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly
85      90      95
Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro
100     105     110
Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg
115     120     125
Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr
130     135     140
Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
145     150     155     160
Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu

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165 170 175  
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 Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg  
 195 200 205  
 Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val Ala Ala Val Leu  
 210 215 220  
 Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala  
 225 230 235 240  
 Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly Thr Ser Ser Lys  
 245 250 255  
 Lys Val Ile Tyr Ser Gln Pro  
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<210> 26  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<400> 26  
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 20 25 30  
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 35 40 45  
 Lys Leu Leu Leu Thr His Thr Glu Arg Val Val Ile Trp Pro Phe Ser  
 50 55 60  
 Asn Lys Asn Tyr Ile His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile  
 65 70 75 80  
 Ser Asn Asn Ala Glu Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu  
 85 90 95  
 Thr Met Ala Asp Asn Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser  
 100 105 110  
 Asp Leu Glu Gly Asn Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val  
 115 120 125  
 Pro Pro Ser Lys Pro Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly  
 130 135 140  
 Asn Asn Ile Gln Leu Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro  
 145 150 155 160  
 Gln Tyr Ser Trp Lys Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu  
 165 170 175  
 Ala Gln Pro Ala Ser Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr  
 180 185 190  
 Asp Thr Ser Gly Tyr Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr  
 195 200 205  
 Gln Phe Cys Asn Ile Thr Val Ala Val Arg Ser Pro Ser Met Asn Val  
 210 215 220  
 Ala Leu Tyr Val Gly Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile  
 225 230 235 240  
 Ile Gly Ile Ile Ile Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn  
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 Thr Glu Asp Lys Glu Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu  
 260 265 270  
 Pro

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<220>

<223> Consensus DNA Sequence

<400> 27

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atcatgtgaa gtacctctt ctgctctgag tggaaactgtg gtagagctac gatgtcaaga 180
caaagaaggg aatccagctc ctgaatacac atggtttaag gatggcatcc gtttgctaga 240
aaatcccaga cttggctccc aaagcaccaa cagctcatac acaatgaata caaaaactgg 300
aactctgcaa ttttaatactg tttccaaact ggacactgga gaatattcct gtgaagcccg 360
caattctgtt ggatatcgca ggtgtcctgg ggaaacgaat gcaagtagat gat 413
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<210> 28

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Primer

<400> 28

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<210> 29

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Primer

<400> 29

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acctgcgata tccaacagaa ttg 23
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<210> 30

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Hybridization Probe

<400> 30

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